

Mon Jul 1 09:26:06 2002

us-09-303-518d-465.rst

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:

June 29, 2002, 22:07:36 ; Search time 17398.4 Seconds
(without alignments)
1296.293 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-303-518D-465
1671

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched:

13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters:

27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:

- 1: em_estba:*
- 2: em_estlm:*
- 3: em_estln:*
- 4: em_estlo:*
- 5: em_estlv:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_hic:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vit:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	165.6	9.9	633	12	AO991398
C 2	44.6	2.7	1025	12	CNS014J2
C 3	42.2	2.5	489	12	AO870477
C 4	41	2.5	1101	12	CNS00LTX
C 5	40.8	2.4	1101	12	CNS00LTX
C 6	40	2.4	878	12	CNS00LTX
C 7	40	2.4	1101	12	CNS00LTX
C 8	39.6	2.4	1101	12	CNS00LTX
C 9	39.4	2.4	651	10	BE846943
C 10	39.4	2.4	1101	12	CNS00LTX
C 11	39.2	2.3	728	10	BE137886
C 12	39	2.3	872	12	BE137886
C 13	39	2.3	872	12	BE137886
C 14	38.6	2.3	842	12	CNS00LTX
C 15	38.6	2.3	842	9	BE188368
C 16	38.6	2.3	947	12	CNS03N8I
C 17	38.6	2.3	962	12	CNS006BI

AV086927 AV086927
 A0494017 HS_5143_B
 A0083062 RBC111-56
 A0866684 nbe0028F
 BF181956 601805387F
 BF430963 B086G58TF
 AL525973 AL525973
 AL5680716 ENMD065TR
 AL398147 T7 end of
 AL182822 Tetradon

ALIGNMENTS

RESULT 1
 A091398/c 633 bp DNA linear GSS 14-AUG-2000
 LOCUS A091398 Photobabidus luminescens strain W14 M13 library
 DEFINITION Photobabidus luminescens genomic clone PLG02325, DNA sequence.

ACCESSION A091398.1 GI:9649992
 VERSION GSS.
 KEYWORDS Photobabidus luminescens.
 SOURCE Photobabidus luminescens.
 ORGANISM Bacteria; Proteobacteria; gamma subdivision; Enderobacteriaceae;
 Photobabidus.

REFERENCE 1 (bases 1 to 633)
 French-Constant, R.H., Waterfield, N., Burland, V., Pena, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R. The complete genome of the entomopathogenic bacterium
 A genomic sample sequence of the entomopathogenic bacterium
 Photobabidus luminescens W14: potential implications for virulence

JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 MEDLINE 20378633
 COMMENT Contact: French-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK

tel: (44) 1225 826621
 fax: (44) 1225 826779
 Email: bsstic@path.ac.uk
 This is one of 2,122 random reads from the M13 library. For
 annotation of identified clones (BLASTX, BLASTN and mapping to E.
 coli K12 genome) please see french-constant et al. 2000, Nucleic
 Acids Res.
 Seq primer: M13 forward
 Class: shotgun.

FEATURES
 source
 1..633
 Location/Qualifiers
 /organism="Photobabidus luminescens"
 /strain="W14"
 /db_xref="taxon:29488"
 /clone="PLG02325"
 /clone_11b="Photobabidus luminescens strain W14 M13
 library"
 /dev_stage="primary phase variant"
 /note="Genomic DNA from strain W14 was size selected (1-2
 kb) and then cloned into M13 Janss." 1 others

BASE COUNT 183 a 152 c 118 g 179 t
 ORIGIN

Query Match 9.9%; Score 165.6; DB 12; Length 633;
 Best Local Similarity 67.9%; Pred. No. 6.8e-34;
 Matches 231; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

1332 tatagatgaacccgcttcttaacggttcgtcgatcgctcatcttctgctcat 1391
 441 TGTGTAAGACGCTCTTTATCTCTGGAATATGCTGCTCATCTTGTGTAAC 382
 1392 aactgcagaaatcaatacgaacaaatacgaagcgaagtaagatacgaatccacc 1451
 381 AAAGCAGAGATTAAGTATGTTGAACCTTCTACGAGAGTAATAATTCCTTATGTTCCGCC 322

1452 taanaattactctcctcagacgcgtaccacaagaccctaataatgatatattgataa 1511
 321 AGAAATTTTCTCCCTCAGCCATTTACCAAGAGACCTTAATATGTTATGATTA 262
 1512 atttgatgaatgagcgaagagcgcacataagaactaagaatgataatgataatgata 1571
 261 ATTGGAATGAATGAGGCTTACGAGGCTTACAGTACTACGAGGCAATCATTCGAGTGGGA 202
 1572 tttcaatgtctctaaacgaag 1631
 201 TGTGACACTATTCGTACCGTAACTCCCACTAAGTTCGATGAGTGGCTACTGATGCGCTCTCA 142
 1632 ttaataatcaattgatgaaagattacacacaatga 1671
 141 TGTGACACTATTCGTATGATGAAATAATATATATAGTGA 102

RESULT 2
 CNS014J2/c 1025 bp DNA linear GSS 26-JUL-1999
 LOCUS CNS014J2 Drosophila melanogaster genome survey sequence T7 end of BAC
 DEFINITION BACN1111 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION AL104216.1 GI:5615827
 VERSION GSS.
 KEYWORDS fruit fly.
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster; Insecta; Hexapoda; Tracheata; Insecta;
 Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1025)
 Genoscope.

AUTHORS Direct Submission
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage;
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail: seque@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
 http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billand at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelBAC11.

FEATURES
 source
 1..1025
 Location/Qualifiers
 /organism="Drosophila melanogaster"
 /plasmid="pBelBAC11"
 /db_xref="taxon:7227"
 /clone_11b="DrosBAC"
 /clone="BACN1111"
 /note="end : 17"

BASE COUNT 148 a 88 c 6 g 522 t 261 others
 ORIGIN

Query Match 2.7%; Score 44.6; DB 12; Length 1025;
 Best Local Similarity 33.3%; Pred. No. 0.65;
 Matches 109; Conservative 57; Mismatches 161; Indels 0; Gaps 0;

1345 gtcttaatcctaaggttcgtcgatcgctcatcttgctctatactgcagaaatt 1404
 764 RTGCTTAATAAATATGTRGTATATATATATATATATATATATATATATATATATATAT 705
 1405 caatacgaataatcacaagcgaagtagaatacagataataccacaaataattact 1464
 704 AAT 645
 1465 ccttaacgacgcgtacccaagagacccaataatgataatgataatgataatgataatgata 1524
 644 GTTKGTRKMAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 585

OY 1525 tggactaaaggtccatcaagaactaaggtccatcaagaatttgatggatgttcattgtct 1584
 DB 584 KGGRTGCGKAKGTTTRDWMWAAAAAAGGCGTGAADARAKGDAA 525
 OY 1585 aaacaagaagaagcaacttgatggctagtgatgtaagattatataca 1644
 DB 524 ARADGRRWAAAAAKRTATKGTGKTGTAGTAAAGATWAAAAAGTTGTVA 465
 OY 1645 attgatgaagattacacacaatga 1671
 DB 464 KWATATTAAAAAATAAAAAAAAKW 438

RESULT 3
 LOCUS A0870477 489 bp DNA linear GSS 03-NOV-1999
 DEFINITION nbe0039G20r CUGI Rice BAC Library (ECORI) Oryza sativa genomic
 ACCESSION A0870477
 VERSION A0870477.1 GI:6220928
 KEYWORDS GSS.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eubartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 489)
 WING, R.A. and DEAN, R.A.
 TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
 JOURNAL Unpublished (1998)
 COMMENT Contact: Ming RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Seq primer: GGAAACAGCTATGACCATG
 Class: BAC ends
 High quality sequence start: 43
 Location/Qualifiers
 1. 489

FEATURES

/organism="Oryza sativa"
 /strain="japonica"
 /cultivar="Nipponbare"
 /db_xref="taxon:4530"
 /clone="nbe0039G20r"
 /clone_lib="CUGI Rice BAC Library (ECORI)"
 /tissue="Leaf"
 /lab_host="E. coli DH10B"
 /note="Vector: PBACindigo; Site 1: EcoRI; Site 2: EcoRI;
 Rice is the most important food crop in the world. Half of
 the world population, especially those inhabiting highly
 populated areas of the humid tropics and subtropics, rely
 on rice as their primary source of carbohydrate.
 Monocotyledonous rice is a diploid plant (2n=24) with a
 haploid genome equivalent of 431 Mbp (Arumuganathan and
 Earle, 1991). The relatively small genome of rice, three
 times larger than that of Arabidopsis, makes it suitable
 for genomic studies. In order to facilitate positional
 cloning, physical mapping and genome sequencing of rice,
 we have constructed a BAC library from Oryza sativa,
 Nipponbare variety using EcoRI as the cloning enzyme. The
 library contains 55,296 clones with an average insert size
 of 121 kb providing approximately 15 haploid genome
 equivalents. The deep coverage allows the isolation a
 particular sequence with a probability of 99.9%. Three
 high density filters, each containing 18,432 clones
 (doubly spotted), represent the whole library for colony
 screening and can be requested from the Clemson University
 BAC/EST Resource Center (www.genome.clemson.edu)."

BASE COUNT 160 a 77 c 85 g 165 t 2 others
 ORIGIN

Query Match 2.5%; Score 42.2; DB 12; Length 489;
 Best Local Similarity 49.3%; Pred. No. 1.9; Length 489;
 Matches 110; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

OY 1449 accataaataactctcctcaagcaccgctacccaagaagcctaataatgatttga 1508
 DB 121 ACTTAACATGGAATTTACATGAGCGCATACCAACCAAAAAACATAGGATCTGCT 180
 OY 1509 taaattggtgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1568
 DB 181 TAAAGTTGAAATTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTA 240
 OY 1569 ggaatgtcaattgtcctaacaagaagaagcaacttgatggctagtgatga 1628
 DB 241 GTTCGATTTGGCAATTAAGATGATGCTAGTCACTTTGCTTGCATTAAGATG 300
 OY 1629 gcatttaataataactcctcctcaagcaccgctacccaagaagcctaataatgatttga 1671
 DB 301 GCCAGATTATACACTTATTTGGAAAAATGAACTTAAGA 343

RESULT 4
 LOCUS CNS00LYB/C 1101 bp DNA linear GSS 14-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence 77 end of BAC:
 BACR4BE18 of RRC1-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL078903.1 GI:5102193
 VERSION AL078903
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1101)
 Genoscope.
 TITLE Direct Submission
 AUTHORS Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage;
 BP 191 91006 Evry cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)
 JOURNAL - Web: www.genoscope.cns.fr
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazuhiro Osoegawa and
 Aaron Mermester in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RRC1-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
 1. 1101
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RRC1-98"
 /clone="BACR4BE18"
 /note="end: 77"
 BASE COUNT 283 a 144 c 202 g 320 t 152 others
 ORIGIN

Query Match 2.5%; Score 41; DB 12; Length 1101;
 Best Local Similarity 31.0%; Pred. No. 6.4;

VERSION	Bu137886.1	GI:18298052
KEYWORDS	EST.	
SOURCE	Caenorhabditis elegans.	
ORGANISM	Caenorhabditis elegans	
REFERENCE	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.	
AUTHORS	1 (bases 1 to 728) Kohara,Y., Shin-I,T., Thierry-Mieg,D., Suzuki,Y. and Sugano,S.	
TITLE	A complementary view of the C.elegans genome	
JOURNAL	Unpublished (2002)	
COMMENT	Contact: Tadasu Shin-I Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855	
FEATURES	Email: tsuhin@genes.nig.ac.jp.	
source	Location/Qualifiers	
	1..728	
	/organism="Caenorhabditis elegans"	
	/strain="N2"	
	/db_xref="taxon:6239"	
	/clone="YK1129C01"	
	/clone_lib="unpublished oligo-capped cDNA library, C.	
	elegans_l1 stage"	
	/sex="hermaphrodite"	
	/tissue.type="whole animal"	
	/dev.stage="l1"	
BASE COUNT	235 a 114 c 174 g 205 t	
ORIGIN		

Query Match	Similarity	2.3%	Score 39.2	DB 10	Length 728
Best Local	Similarity	46.6%	Pred. No. 16		
Matches 125	Conservative	0	Mismatches 143	Indels	Gaps 0
QY	1401	aattcaatacagaaattaccaggccaagtgaatcagatatcccaactaaatla	1460		
DB	4	AATTATTGAGTAACACACAAAATGTGTAATACAGAAAGACCTCATGAACGTATG	63		
QY	1461	ctctccctcgaaccgcgtaccaaaaggacctataatgtgataatttgataaatttgtaa	1520		
DB	64	ACTGCTTGAATTAATATTATTGATGATATATATAAATGTTGAAAAGTAAATGAGAGA	123		
QY	1521	tgaatgagactaaaggtccatcaagaactaaagttcaagaatttgatgagatgttcatt	1580		
DB	124	TGAACGGATTACCGAATTCAAACAAATTATGTGGATTAAACAGAGATGGATGTAT	183		
QY	1581	gctctaaacaggaagaagagcaacttggatgggctgtaggagtgtgtaacatctaataat	1640		
DB	184	CTATTAATTAAATTAATGATCATGTTGATGAGCTGGAAACGAACAGATTTGATGT	243		
QY	1641	atcaatttgatggaagattaccacacaa	1668		
DB	244	GTCGTATAGGTGTGGTAAATAAGAGA	271		
RESULT 12	BH233657/c				
LOCUS	1006175A01.y1	1006	- Rescuedu Grid G Zea mays genomic.	DNA	linear
DEFINITION	BH233657	572 bp			GSS 08-NOV-2006
ACCESSION	BH233657				
VERSION	BH233657.1	GI:16840112			
KEYWORDS	GSS.				
SOURCE	Zea mays.				
ORGANISM	Zea mays				
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 572)				
	Walbot,V.				

TITLE	Maize genomic sequences found using engineered RescuemU transposon
JOURNAL	Unpublished (2001)
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8321 Email: walbot@stanford.edu Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately. plate: 1006175 row: 25 class: transposon-tagged. location/Qualifiers 1..572
FEATURES	
source	

Query Match	Best Local Similarity	Score	DB	Length	572;
Matches	84; Conservative	0;	Mismatches	75;	Indels
					Gaps
					0;
Qy 658	gccgcgcgaagcttccaagcagctgcagatatacgtaaaacatcatcgcgcgagga	717			
Ddb 550	GACGCGCGCGCATATGCGAGTCCGACGATCGTCACATGATCATGAGAGCCTGCGCGT	491			
Qy 718	gaatatgtcgagcgagcgatcgctgcagggatataagcgaaaggtccaacatgtctgt	777			
Ddb 490	GAAGAGCGGCGCGCGAGCGTGGACGCTGCTGCTCCCGACGACCCCTACGAGCGCGCC	431			
Qy 778	atgcacgagcttggtgctgcttccacacgaacaaagatg	816			
Ddb 430	ATGCAACCGCTTCTGACGCCCTTCATCGACGACAAAGTGTG	392			
RESULT 13					
LOCUS B1957771					
DEFINITION	B1957771	872 bp	mRNA	linear	EST 22-OCT-2001
ACCESSION	HVSMEN0011B17f				rescue library HVCN0A0015
VERSION	B1957771				(normal) Hordeum vulgare cDNA clone HVSMEN0011B17f, mRNA sequence.
KEYWORDS	B1957771.1	GI:16309026			
SOURCE	EST.				
ORGANISM	Hordeum vulgare				
	barley.				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
	Triticeae; Hordeum.				
REFERENCE	1 (bases 1 to 872)				
AUTHORS	Wing,R., Close,T.J., Kleinof,A., Wise,R., Chin,A., Begum,D.,				
	Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,				
	J., Oates,R. and Main,D.				
TITLE	Development of a genetically and physically anchored EST resource				

JOURNAL
COMMENT

for barley genomics: Morex rachis cDNA library

Unpublished (2001)

Contact: Wing RA

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hg bases = 357

Seq primer: AATTACCTCCTACTAAGG

High quality sequence start: 800.

High quality sequence stop: 800.

FEATURES
SOURCE

1. 872

/organism="Hordeum vulgare"

/cultivar="Morex"

/db_xref="taxon:4513"

/clone="HVMEN001B17f"

/clone_lib="Hordeum vulgare rachis EST library HVCNDA0015

(normal)"

/tissue_type="Rachis"

/lab_host="rjcl21"

/note="Vector: Bluescript SK(-); Site-1: EcoRI; Site-2:

XhoI; Plants were grown at Washington State University,

Pullman, WA in a greenhouse, the rachises were excised and

frozen in liquid nitrogen (Kleinof's lab). In the T1 close

lab at the University of California, Riverside total RNA

was prepared: poly(A) was purified, one primary

unamplified cDNA library was made, and 1 million pfu were

in vitro excised to give phagescript SK(-) cDNA phagemids

(Chin). Phagemids were plated and picked at the Clemson

University Genomics Institute (CUGI) (Begum, Palmer,

Frisch, Atkins and Wing). Plasmid DNA preparations, DNA

sequencing and sequence analysis were performed at CUGI

(Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The

sequence has been trimmed to remove vector sequence and

contains a minimum of 100 bases of phred value 20 or

above. For more details on library preparation and

sequence analysis see

http://www.genome.clemson.edu/projects/barley. To order

this clone see http://www.genome.clemson.edu/orders Also

see clone T1, Wing R, Kleinof's A, Wise R (2001)

Genetically and physically anchored EST resources for

barley genomics. Barley Genetics Newsletter 31:29-30.

(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 206 a 273 c 280 g 113 t

BASE COUNT
ORIGIN

Query Match 2.3%; Score 39; DB 10; Length 872;

Best Local Similarity 68.4%; Pred. No. 20;

Matches 54; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 387 ccattggagcgtacgaacacacccgcgcgcgtatgagggcccaagcgcgcg 446

DB 637 CCACGACGACGAGAGCAAAAGCATGCCGCCGCTACGGCGCAATGATGTCAG 696

QY 447 ctatccgcgtcccaagcg 465

DB 697 GAATCCCGTCCACACAGC 715

RESULT 14

CNS07ECR

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

643 bp DNA linear GSS 08-JUL-2001

T7 end of clone XBDNA002H12 of library XBDNA from strain CBS 94

of Candida tropicalis, genomic survey sequence.

AL441601

AL441601.1 GI:12224827

GSS.

Candida tropicalis.

Candida tropicalis

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

Eukaryota: Fungi: Ascomycota; Saccharomycotina: Saccharomycetes;

Saccharomycetales; mitospotic Saccharomycetales; Candida.

1 (bases 1 to 643)

Blandin,G., Ozler-Kalogeropoulos,O., Winkler,P., Artiguenave,F. and

Dujon,B.

Genomic exploration of the hemiascomycetous yeasts: 16. Candida

tropicalis

FEMS Lett. 487 (1), 91-94 (2000)

20584726

2 (bases 1 to 643)

Soucié,J.L., Aigle,M., Artiguenave,F., Blandin,G.,

Bolotin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S.,

de-Montigny,J., Dujon,B., Durieux,P., Lepingle,A., Llorente,B.,

Malpertuy,A., Neveglise,C., Ozler-Kalogeropoulos,O., Potier,S.,

Saurin,M., Tekala,F., Toffano-Nicche,C., Wesolowski-Louvel,M.,

Winkler,P. and Weissendach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

FEMS Lett. 487 (1), 3-12 (2000)

20584711

3 (bases 1 to 643)

Genoscope.

Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :

segrefgenoscope.cns.fr - Web :

This GSS is part of a random genomic sequencing program of thirteen

yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,

Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to

5 Kb were prepared and both extremities were sequenced. See

keywords for description of this sequence and for the sequence of

the other extremity of this insert.

Location/Qualifiers

1. 643

/organism="Candida tropicalis"

/strain="CBS 94"

/db_xref="taxon:5482"

/clone="XBDNA002H12"

/clone_lib="XBDNA"

/note="end : 77"

BASE COUNT 226 a 107 c 131 g 155 t 24 others

ORIGIN

Query Match 2.3%; Score 38.6; DB 12; Length 643;

Best Local Similarity 52.6%; Pred. No. 21;

Matches 71; Conservative 5; Mismatches 59; Indels 0; Gaps 0;

QY 1194 aaagcgaagatgtgaactgcaaacacgcgcacccgaagcgaagtgccgttga 1253

DB 211 AAGACAAAGAAAGCAAAATAGCAAGCAATTAATAAAATCTAATAGAGATTTT 270

QY 1254 cgttaaaggttctcgaatttgaataaagcgttaataatagatacgataatgaacgc 1313

DB 271 TGTATATAATTTTTCATCTTTTWTAGMCCGGAATFACCTAATAATGAATACCTA 330

QY 1314 tttaccacaagtga 1328

DB 331 TACAATAATTAAGAA 345

RESULT 15

BE188368

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

EST.

842 bp mRNA linear EST 12-MAR-2001

PVB 154 L99-22 Litopenaeus vannamei cDNA similar to Peptidyl-prolyl

cis-trans Isomerase, mRNA sequence.

BE188368

BE188368.1 GI:8888568

EST.

FEATURES	source
REFERENCE	1. 884
AUTHORS	/organism="Hordeum vulgare"
JOURNAL	/cultivar="Morex"
COMMENT	/db_xref="taxon:4513"
	/clone="HVSME0003K24f"
	Location/Qualifiers
	High quality sequence stop: 415.
	Seq primer: AATTAACCTCCTCAATAAGCG
	Total bp bases = 262
	Email: rwing@clemons.edu
	Fax: 864 656 4293
	Tel: 864 656 7288
	100 Jordan Hall, Clemson, SC 29634, USA
	Clemson University
	Contact: Wing RA
	Unpublished (2001)
TITLE	Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library
REFERENCE	1 (bases 1 to 884)
AUTHORS	Wing, R., Close, T.J., Kleinbols, A., Wise, R., Chin, A., Begum, D., Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., and Main, D.
JOURNAL	Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library
COMMENT	Unpublished (2001)
	Triticaceae: Hordeum.
	Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Pooideae
	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
	Hordeum vulgare
	barley.
	EST.
	BI956488.1 GI:16307741
	BI956488
	(normal) Hordeum vulgare cDNA clone HVSME0003K24f, mRNA sequence.
	HVSME0003K24f Hordeum vulgare rachis EST library HVCN0015
	884 bp mRNA linear EST 22-OCT-2001
	BI956488
	LOCUS
	DEFINITION
	ACCESSION
	VERSION
	KEYWORDS
	SOURCE
	ORGANISM
	Hordeum vulgare
	barley.
	EST.
	BI956488.1 GI:16307741
	BI956488
	(normal) Hordeum vulgare cDNA clone HVSME0003K24f, mRNA sequence.
	HVSME0003K24f Hordeum vulgare rachis EST library HVCN0015
	884 bp mRNA linear EST 22-OCT-2001
	BI956488
	LOCUS
	DEFINITION
	ACCESSION
	VERSION
	KEYWORDS
	SOURCE
	ORGANISM
	Hordeum vulgare
	barley.
	EST.
	BI956488.1 GI:16307741
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	(normal) Hordeum vulgare cDNA clone HVSME0003K24f, mRNA sequence.
	HVSME0003K24f Hordeum vulgare rachis EST library HVCN0015
	884 bp mRNA linear EST 22-OCT-2001
	BI956488
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	ORGANISM
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	HVSME0003K24f Hordeum vulgare rachis EST library HVCN0015
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	SOURCE
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	EST.
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	(normal) Hordeum vulgare cDNA clone HVSME0003K24f, mRNA sequence.
	HVSME0003K24f Hordeum vulgare rachis EST library HVCN0015
	884 bp mRNA linear EST 22-OCT-2001
	BI956488
	LOCUS
	DEFINITION
	ACCESSION
	VERSION
	KEYWORDS
	SOURCE
	ORGANISM
	Hordeum vulgare
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	EST.
	BI956488.1 GI:16307741
	BI956488
	(normal) Hordeum vulgare cDNA clone HVSME0003K24f, mRNA sequence.
	HVSME0003K24f Hordeum vulgare rachis EST library HVCN0015
	884 bp mRNA linear EST 22-OCT-2001
	BI956488
	LOCUS
	DEFINITION
	ACCESSION
	VERSION
	KEYWORDS
	SOURCE
	ORGANISM
	Hordeum vulgare
	barley.
	EST.
	BI956488.1 GI:16307741
	BI956488
	(normal) Hordeum vulgare cDNA clone HVSME0003K24f, mRNA sequence.
	HVSME0003K24f Hordeum vulgare rachis EST library HVCN0015
	884 bp mRNA linear EST 22-OCT-2001
	BI956488
	LOCUS
	DEFINITION
	ACCESSION
	VERSION
	KEYWORDS
	SOURCE

Email: bjortus@tigr.org
Clones are derived from the *Entamoeba histolytica* HMI:IMSS sheared

Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, J.G. M.

COMMENT

Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@igir.org
Clones are derived from the *Entamoeba histolytica* HM1:IMSS sheared
DNA library
Seq primer: M3-Forward
Class: shotgun
High quality sequence start: 15
High quality sequence stop: 687.

FEATURES
source

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/organism="Entamoeba histolytica"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/vector="pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broch cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, I.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

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RESULT 36

Accession	Version	Keywords	Source	Organism	Reference
CNS03B69					
CNS03B69					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					

Query Match	2.2%	Score 37.2	DB 12	Length 967
Best Local Similarity	20.3%	Pred. No. 64		
Matches 65	Conservative 116	Mismatches 139	Indels 0	Gaps 0
QY	1347	ctttaactcctaagaaggtctgtcgcatacgcctcatcttgcgtcataactccagaattca	1406	
Db	966	vtktsmctygcgcaavdrcscitmbmtsasbknkmsommacabrcraammmvmttmattnra	907	
QY	1407	atagcgaataattcccaagcgaagtgatgaatcagatatccacccataaatactctcc	1466	
Db	906	ahnmamarrrmttroggrykkavragwmsrcthtntvmtsmbsbcscktdvrsavmmvaaav	847	
QY	1467	ttcagaccscgtaccaaagaagcctaataatgatatttgatattggataattggtaataag	1526	
Db	846	rkmrtrhmmvttttacabamgvsasccgvkxvsttvtswcnsmtcgvncvncmtrraaw	787	
QY	1527	gactaaaggtcatcataagaactaaagtgataagaatttgatggatgtcataactgtctaa	1586	
Db	786	vdmhrraavtamhttmmtatagatammmttsrmtavtttnnavtdtlatwhtttammmvtagaa	727	
QY	1587	aacaggaagaagcgaacttgatggcgctagtgtggatgtaagcatttaataataatcaat	1646	
Db	726	matssmcmcdmymcvcckkvmgncscctcvbksGCCBkvvtdwvktttvmmvmtttaca	667	
QY	1647	tgatgaagaattacacaca	1666	
Db	666	caatnrcmrsttttctcrda	647	
RESULT 39				
CNS0204B				
LOCUS	CNS0204B	997 bp	DNA	linear
DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 221B20 of library G from Tetraodon nigroviridis, genomic survey sequence.			
ACCESSION	AL175124	GI:7813181		
VERSION	AL175124.1			
KEYWORDS	GSS: genome survey sequence.			
SOURCE	Tetraodon nigroviridis.			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.			
REFERENCE	1 (bases 1 to 997)			
AUTHORS	Roest-Croliius,H., Jallion,O., Dasilva,C., Flzames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.			
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis			
JOURNAL	unpublished			
REFERENCE	2 (bases 1 to 997)			
AUTHORS	Roest-Croliius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,			

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
Pterygota; Neoptera; Endopterygota; Diptera: Brachycera:

